

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: LEUNG, David W.
TOMPKINS, Christopher K.
- (ii) TITLE OF INVENTION: HUMAN PHOSPHATIDIC ACID PHOSPHATASE
- (iii) NUMBER OF SEQUENCES: 21
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Foley & Lardner
 - (B) STREET: 3000 K Street, N.W., Suite 500
 - (C) CITY: Washington
 - (D) STATE: D.C.
 - (E) COUNTRY: USA
 - (F) ZIP: 20007-5109
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/842,827
 - (B) FILING DATE: 17-APR-1997
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: BENT, Stephen A.
 - (B) REGISTRATION NUMBER: 29,768
 - (C) REFERENCE/DOCKET NUMBER: 77319/125
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (202)672-5300
 - (B) TELEFAX: (202)672-5399
 - (C) TELEX: 904136

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1563 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 342..1193
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 342..1193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCTGTGGGAG AGAGCGCCGG GATCCGGACG GGGTAGCAAC CGGGGCAGGC CGTGCCGGCT	60
GAGGAGGTCC TGAGGGCTACA GAGCTGCCGC GGCTGGCACA CGAGGCCCTC GGCACTAAC	120

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GAGTGTTCGC	GGGGGCTGTG	AGGGGAGGGC	CCCGGGCGCC	ATTGCTGGCG	GTGGGAGCGC	180
CGCCCGGTCT	CAGCCCGCCC	TCGGCTGCTC	TCCTCCTCCG	GCTGGGAGGG	GCCGTATCTC	240
GGGGCCGTCG	CCAGCCCCGG	CCCGGGCTCG	ATAATCAAGG	GCCTCGGCCG	TCGTCCCGCA	300
CCTCATTCCA	TCGCCCTTGC	CGGGCAGCCC	GGGCAGAGAC	C ATG TTT GAC AAG		353
				Met Phe Asp Lys		
				1		
ACG CGG CTG CCG TAC GTG GCC CTC GAT GTG CTC TGC GTG TTG CTG GCT						401
Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Leu Cys Val Leu Leu Ala						
5	10		15		20	
GGA TTG CCT TTT GCA ATT CTT ACT TCA AGG CAT ACC CCC TTC CAA CGA						449
Gly Leu Pro Phe Ala Ile Leu Thr Ser Arg His Thr Pro Phe Gln Arg						
25	30		35			
GGA GTA TTC TGT AAT GAT GAG TCC ATC AAG TAC CCT TAC AAA GAA GAC						497
Gly Val Phe Cys Asn Asp Glu Ser Ile Lys Tyr Pro Tyr Lys Glu Asp						
40	45		50			
ACC ATA CCT TAT GCG TTA TTA GGT GGA ATA ATC ATT CCA TTC AGT ATT						545
Thr Ile Pro Tyr Ala Leu Leu Gly Gly Ile Ile Ile Pro Phe Ser Ile						
55	60		65			
ATC GTT ATT ATT CTT GGA GAA ACC CTG TCT GTT TAC TGT AAC CTT TTG						593
Ile Val Ile Ile Leu Gly Glu Thr Leu Ser Val Tyr Cys Asn Leu Leu						
70	75		80			
CAC TCA AAT TCC TTT ATC AGG AAT AAC TAC ATA GCC ACT ATT TAC AAA						641
His Ser Asn Ser Phe Ile Arg Asn Asn Tyr Ile Ala Thr Ile Tyr Lys						
85	90		95		100	
GCC ATT GGA ACC TTT TTA TTT GGT GCA GCT GCT AGT CAG TCC CTG ACT						689
Ala Ile Gly Thr Phe Leu Phe Gly Ala Ala Ser Gln Ser Leu Thr						
105	110		115			
GAC ATT GCC AAG TAT TCA ATA GGC AGA CTG CGG CCT CAC TTC TTG GAT						737
Asp Ile Ala Lys Tyr Ser Ile Gly Arg Leu Arg Pro His Phe Leu Asp						
120	125		130			
GTT TGT GAT CCA GAT TGG TCA AAA ATC AAC TGC AGC GAT GGT TAC ATT						785
Val Cys Asp Pro Asp Trp Ser Lys Ile Asn Cys Ser Asp Gly Tyr Ile						
135	140		145			
GAA TAC TAC ATA TGT CGA GGG AAT GCA GAA AGA GTT AAG GAA GGC AGG						833
Glu Tyr Tyr Ile Cys Arg Gly Asn Ala Glu Arg Val Lys Glu Gly Arg						
150	155		160			
TTG TCC TTC TAT TCA GGC CAC TCT TCG TTT TCC ATG TAC TGC ATG CTG						881
Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Ser Met Tyr Cys Met Leu						
165	170		175		180	
TTT GTG GCA CTT TAT CTT CAA GCC AGG ATG AAG GGA GAC TGG GCA AGA						929
Phe Val Ala Leu Tyr Leu Gln Ala Arg Met Lys Gly Asp Trp Ala Arg						
185	190		195			
CTC TTA CGC CCC ACA CTG CAA TTT GGT CTT GTT GCC GTA TCC ATT TAT						977
Leu Leu Arg Pro Thr Leu Gln Phe Gly Leu Val Ala Val Ser Ile Tyr						
200	205		210			
GTG GGC CTT TCT CGA GTT TCT GAT TAT AAA CAC CAC TGG AGC GAT GTG						1025
Val Gly Leu Ser Arg Val Ser Asp Tyr Lys His His Trp Ser Asp Val						
215	220		225			

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TTG ACT GGA CTC ATT CAG GGA GCT CTG GTT GCA ATA TTA GTT GCT GTA Leu Thr Gly Leu Ile Gln Gly Ala Leu Val Ala Ile Leu Val Ala Val 230 235 240	1073
TAT GTA TCG GAT TTC TTC AAA GAA AGA ACT TCT TTT AAA GAA AGA AAA Tyr Val Ser Asp Phe Phe Lys Glu Arg Thr Ser Phe Lys Glu Arg Lys 245 250 255 260	1121
GAG GAG GAC TCT CAT ACA ACT CTG CAT GAA ACA CCA ACA ACT GGG AAT Glu Glu Asp Ser His Thr Thr Leu His Glu Thr Pro Thr Thr Gly Asn 265 270 275	1169
CAC TAT CCG AGC AAT CAC CAG CCT TGAAAGGCAG CAGGGTGCCC AGGTGAAGCT His Tyr Pro Ser Asn His Gln Pro 280	1223
GGCCTGTTT CTAAGGAAA ATGATTGCCA CAAGGCAAGA GGATGCATCT TTCTTCCTGG TGTACAAGCC TTTAAAGACT TCTGCTGCTG ATATGCCTCT TGGATGCACA CTTTGTGTGT ACATAGTTAC CTTTAACCTCA GTGGTTATCT AATAGCTCTA AACTCATTAA AAAAAGTCCA AGCCTTCCAC CAAAACAGTG CCCCCACCTGT ATACATTTT ATTAAAAAAA TGTAATGCTT ATGTATAAAC ATGTATGTAA TATGCTTCT ATGAATGATG TTTGATTAA ATATAATACA TATTAAGGAGAA CCAAAAAAA AAAAAAAA	1283 1343 1403 1463 1523 1563

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 284 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Phe Asp Lys Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Leu Cys 1 5 10 15
Val Leu Leu Ala Gly Leu Pro Phe Ala Ile Leu Thr Ser Arg His Thr 20 25 30
Pro Phe Gln Arg Gly Val Phe Cys Asn Asp Glu Ser Ile Lys Tyr Pro 35 40 45
Tyr Lys Glu Asp Thr Ile Pro Tyr Ala Leu Leu Gly Gly Ile Ile Ile 50 55 60
Pro Phe Ser Ile Ile Val Ile Ile Leu Gly Glu Thr Leu Ser Val Tyr 65 70 75 80
Cys Asn Leu Leu His Ser Asn Ser Phe Ile Arg Asn Asn Tyr Ile Ala 85 90 95
Thr Ile Tyr Lys Ala Ile Gly Thr Phe Leu Phe Gly Ala Ala Ala Ser 100 105 110
Gln Ser Leu Thr Asp Ile Ala Lys Tyr Ser Ile Gly Arg Leu Arg Pro 115 120 125
His Phe Leu Asp Val Cys Asp Pro Asp Trp Ser Lys Ile Asn Cys Ser 130 135 140

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Asp Gly Tyr Ile Glu Tyr Tyr Ile Cys Arg Gly Asn Ala Glu Arg Val
145 150 155 160
Lys Glu Gly Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Ser Met
165 170 175
Tyr Cys Met Leu Phe Val Ala Leu Tyr Leu Gln Ala Arg Met Lys Gly
180 185 190
Asp Trp Ala Arg Leu Leu Arg Pro Thr Leu Gln Phe Gly Leu Val Ala
195 200 205
Val Ser Ile Tyr Val Gly Leu Ser Arg Val Ser Asp Tyr Lys His His
210 215 220
Trp Ser Asp Val Leu Thr Gly Leu Ile Gln Gly Ala Leu Val Ala Ile
225 230 235 240
Leu Val Ala Val Tyr Val Ser Asp Phe Phe Lys Glu Arg Thr Ser Phe
245 250 255
Lys Glu Arg Lys Glu Glu Asp Ser His Thr Thr Leu His Glu Thr Pro
260 265 270
Thr Thr Gly Asn His Tyr Pro Ser Asn His Gln Pro
275 280

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1566 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 342..1196
(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 342..1196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCTGTGGGAG AGAGCGCCGG GATCCGGACG GGGTAGCAAC CGGGGCAGGC CGTGCCGGCT 60
GAGGAGGTCC TGAGGCTACA GAGCTGCCGC GGCTGGCACCA CGAGCGCCTC GGCACTAACC 120
GAGTGTTCGC GGGGGCTGTG AGGGGAGGGC CCCGGGCGCC ATTGCTGGCG GTGGGAGCGC 180
CGCCCGGTCT CAGCCCGCCC TCGGCTGCTC TCCTCCTCCG GCTGGGAGGG GCCGTATCTC 240
GGGGCCGTCG CCAGCCCCGG CCCGGGCTCG ATAATCAAGG GCCTCGGCCG TCGTCCCGCA 300
CCTCATTCCA TCGCCCTTGC CGGGCAGCCC GGGCAGAGAC C ATG TTT GAC AAG 353
Met Phe Asp Lys
1
ACG CGG CTG CCG TAC GTG GCC CTC GAT GTG CTC TGC GTG TTG CTG GCT 401
Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Leu Cys Val Leu Leu Ala
5 10 15 20

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-5-

TCC ATG CCT ATG GCT GTT CTA AAA TTG GGC CAA ATA TAT CCA TTT CAG Ser Met Pro Met Ala Val Leu Lys Leu Gly Gln Ile Tyr Pro Phe Gln 25 30 35	449
AGA GGC TTT TTC TGT AAA GAC AAC AGC ATC AAC TAT CCG TAC CAT GAC Arg Gly Phe Phe Cys Lys Asp Asn Ser Ile Asn Tyr Pro Tyr His Asp 40 45 50	497
AGT ACC GCC GCA TCC ACT GTC CTC ATC CTA GTG GGG GTT GGC TTG CCC Ser Thr Ala Ala Ser Thr Val Leu Ile Leu Val Gly Val Gly Leu Pro 55 60 65	545
GTT TCC TCT ATT ATT CTT GGA GAA ACC CTG TCT GTT TAC TGT AAC CTT Val Ser Ser Ile Ile Leu Gly Glu Thr Leu Ser Val Tyr Cys Asn Leu 70 75 80	593
TTG CAC TCA AAT TCC TTT ATC AGT AAT AAC TAC ATA GCC ACT ATT TAC Leu His Ser Asn Ser Phe Ile Ser Asn Asn Tyr Ile Ala Thr Ile Tyr 85 90 95 100	641
AAA GCC ATT GGA ACC TTT TTA TTT GGT GCA GCT GCT AGT CAG TCC CTG Lys Ala Ile Gly Thr Phe Leu Phe Gly Ala Ala Ser Gln Ser Leu 105 110 115	689
ACT GAC ATT GCC AAG TAT TCA ATA GGC AGA CTG CGG CCT CAC TTC TTG Thr Asp Ile Ala Lys Tyr Ser Ile Gly Arg Leu Arg Pro His Phe Leu 120 125 130	737
GAT GTT TGT GAT CCA GAT TGG TCA AAA ATC AAC TGC AGC GAT GGT TAC Asp Val Cys Asp Pro Asp Trp Ser Lys Ile Asn Cys Ser Asp Gly Tyr 135 140 145	785
ATT GAA TAC TAC ATA TGT CGA GGG AAT GCA GAA AGA GTT AAG GAA GGC Ile Glu Tyr Tyr Ile Cys Arg Gly Asn Ala Glu Arg Val Lys Glu Gly 150 155 160	833
AGG TTG TCC TTC TAT TCA GGC CAC TCT TCG TTT TCC ATG TAC TGC ATG Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Ser Met Tyr Cys Met 165 170 175 180	881
CTG TTT GTG GCA CTT TAT CTT CAA GCC AGG ATG AAG GGA GAC TGG GCA Leu Phe Val Ala Leu Tyr Leu Gln Ala Arg Met Lys Gly Asp Trp Ala 185 190 195	929
AGA CTC TTA CGC CCC ACA CTG CAA TTT GGT CTT GTT GCC GTA TCC ATT Arg Leu Leu Arg Pro Thr Leu Gln Phe Gly Leu Val Ala Val Ser Ile 200 205 210	977
TAT GTG GGC CTT TCT CGA GTT TCT GAT TAT AAA CAC CAC TGG AGC GAT Tyr Val Gly Leu Ser Arg Val Ser Asp Tyr Lys His His Trp Ser Asp 215 220 225	1025
GTG TTG ACT GGA CTC ATT CAG GGA GCT CTG GTT GCA ATA TTA GTT GCT Val Leu Thr Gly Leu Ile Gln Gly Ala Leu Val Ala Ile Leu Val Ala 230 235 240	1073
GTA TAT GTA TCG GAT TTC TTC AAA GAA AGA ACT TCT TTT AAA GAA AGA Val Tyr Val Ser Asp Phe Phe Lys Glu Arg Thr Ser Phe Lys Glu Arg 245 250 255 260	1121
AAA GAG GAG GAC TCT CAT ACA ACT CTG CAT GAA ACA CCA ACA ACT GGG Lys Glu Glu Asp Ser His Thr Thr Leu His Glu Thr Pro Thr Thr Gly 265 270 275	1169
AAT CAC TAT CCG AGC AAT CAC CAG CCT TGAAAGGCAG CAGGGTGCCC Asn His Tyr Pro Ser Asn His Gln Pro 280 285	1216

AGGTGAAGCT GGCCTGTTT CAAAGGAAA ATGATTGCCA CAAGGCAAGA GGATGCATCT	1276
TTCTTCCTGG TGTACAAGCC TTTAAAGACT TCTGCTGCTG ATATGCCTCT TGGATGCACA	1336
CTTTGTGTGT ACATAGTTAC CTTTAACCTCA GTGGTTATCT AATAGCTCTA AACTCATTAA	1396
AAAAACTCCA AGCCTTCCAC CAAACACAGTG CCCCACCTGT ATACATTTTT ATTAAAAAAA	1456
TGTAATGCTT ATGTATAAAC ATGTATGTAA TATGCTTCT ATGAATGATG TTTGATTTAA	1516
ATATAATACA TATTAATATG TATGGGAGAA CCAAAAAAAA AAAAAAAA	1566

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 285 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Phe Asp Lys Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Leu Cys	
1 5 10 15	
Val Leu Leu Ala Ser Met Pro Met Ala Val Leu Lys Leu Gly Gln Ile	
20 25 30	
Tyr Pro Phe Gln Arg Gly Phe Phe Cys Lys Asp Asn Ser Ile Asn Tyr	
35 40 45	
Pro Tyr His Asp Ser Thr Ala Ala Ser Thr Val Leu Ile Leu Val Gly	
50 55 60	
Val Gly Leu Pro Val Ser Ser Ile Ile Leu Gly Glu Thr Leu Ser Val	
65 70 75 80	
Tyr Cys Asn Leu Leu His Ser Asn Ser Phe Ile Ser Asn Asn Tyr Ile	
85 90 95	
Ala Thr Ile Tyr Lys Ala Ile Gly Thr Phe Leu Phe Gly Ala Ala Ala	
100 105 110	
Ser Gln Ser Leu Thr Asp Ile Ala Lys Tyr Ser Ile Gly Arg Leu Arg	
115 120 125	
Pro His Phe Leu Asp Val Cys Asp Pro Asp Trp Ser Lys Ile Asn Cys	
130 135 140	
Ser Asp Gly Tyr Ile Glu Tyr Tyr Ile Cys Arg Gly Asn Ala Glu Arg	
145 150 155 160	
Val Lys Glu Gly Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Ser	
165 170 175	
Met Tyr Cys Met Leu Phe Val Ala Leu Tyr Leu Gln Ala Arg Met Lys	
180 185 190	
Gly Asp Trp Ala Arg Leu Leu Arg Pro Thr Leu Gln Phe Gly Leu Val	
195 200 205	
Ala Val Ser Ile Tyr Val Gly Leu Ser Arg Val Ser Asp Tyr Lys His	
210 215 220	

His Trp Ser Asp Val Leu Thr Gly Leu Ile Gln Gly Ala Leu Val Ala
 225 230 235 240

Ile Leu Val Ala Val Tyr Val Ser Asp Phe Phe Lys Glu Arg Thr Ser
 245 250 255

Phe Lys Glu Arg Lys Glu Glu Asp Ser His Thr Thr Leu His Glu Thr
 260 265 270

Pro Thr Thr Gly Asn His Tyr Pro Ser Asn His Gln Pro
 275 280 285

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 294..1226

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 294..1226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGCGCAGCTC TGCAAAAGTT TCTGCTCGGG ATCTGGCTCT CTTCCCTTG GACTTTAGAA 60

CGATTTAGGG TTGACAGAGG AAAGCAGAGG CGCGCAGGAG GAGCAGAAAA CACCACCTTC 120

TGCAGTTGGA GGCAGGCAGC CCCGGCTGCA CTCTAGCCGC CGCGCCCGGA GCCGGGGCCG 180

ACCCGCCACT ATCCGCAGCA GCCTCGGCCA GGAGGCGACC CGGGCGCCTG GGTGTGTGGC 240

TGCTGTTGCG GGACGTCTTC GCAGGGCGGG AGGCTCGCGC CGCAGCCAGC GCC ATG 296
 Met
 1

CAA AAC TAC AAG TAC GAC AAA GCG ATC GTC CCG GAG AGC AAG AAC GGC 344
 Gln Asn Tyr Lys Tyr Asp Lys Ala Ile Val Pro Glu Ser Lys Asn Gly
 5 10 15

GCG AGC CCG GCG CTC AAC AAC CCG AGG AGG AGC GGC AGC AAG CGG 392
 Gly Ser Pro Ala Leu Asn Asn Pro Arg Arg Ser Gly Ser Lys Arg
 20 25 30

GTG CTG CTC ATC TGC CTC GAC CTC TTC TGC CTC TTC ATG GCG GGC CTC 440
 Val Leu Leu Ile Cys Leu Asp Leu Phe Cys Leu Phe Met Ala Gly Leu
 35 40 45

CCC TTC CTC ATC ATC GAG ACA AGC ACC ATC AAG CCT TAC CAC CGA GGG 488
 Pro Phe Leu Ile Ile Glu Thr Ser Thr Ile Lys Pro Tyr His Arg Gly
 50 55 60 65

TTT TAC TGC AAT GAT GAG AGC ATC AAG TAC CCA CTG AAA ACT GGT GAG 536
 Phe Tyr Cys Asn Asp Glu Ser Ile Lys Tyr Pro Leu Lys Thr Gly Glu
 70 75 80

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ACA ATA AAT GAC GCT GTG CTC TGT GCC GTG GGG ATC GTC ATT GCC ATC Thr Ile Asn Asp Ala Val Leu Cys Ala Val Gly Ile Val Ile Ala Ile 85 90 95	584
CTC GCG ATC ATC ACG GGG GAA TTC TAC CGG ATC TAT TAC CTG AAG AAG Leu Ala Ile Ile Thr Gly Glu Phe Tyr Arg Ile Tyr Tyr Leu Lys Lys 100 105 110	632
TCG CGG TCG ACG ATT CAG AAC CCC TAC GTG GCA GCA CTC TAT AAG CAA Ser Arg Ser Thr Ile Gln Asn Pro Tyr Val Ala Ala Leu Tyr Lys Gln 115 120 125	680
GTG GGC TGC TTC CTC TTT GGC TGT GCC ATC AGC CAG TCT TTC ACA GAC Val Gly Cys Phe Leu Phe Gly Cys Ala Ile Ser Gln Ser Phe Thr Asp 130 135 140 145	728
ATT GCC AAA GTG TCC ATA GGG CGC CTG CGT CCT CAC TTC TTG AGT GTC Ile Ala Lys Val Ser Ile Gly Arg Leu Arg Pro His Phe Leu Ser Val 150 155 160	776
TGC AAC CCT GAT TTC AGC CAG ATC AAC TGC TCT GAA GGC TAC ATT CAG Cys Asn Pro Asp Phe Ser Gln Ile Asn Cys Ser Glu Gly Tyr Ile Gln 165 170 175	824
AAC TAC AGA TGC AGA GGT GAT GAC AGC AAA GTC CAG GAA GCC AGG AAG Asn Tyr Arg Cys Arg Gly Asp Asp Ser Lys Val Gln Glu Ala Arg Lys 180 185 190	872
TCC TTC TCT GGC CAT GCC TCC TTC TCC ATG TAC ACT ATG CTG TAT Ser Phe Ser Gly His Ala Ser Phe Ser Met Tyr Thr Met Leu Tyr 195 200 205	920
TTG GTG CTA TAC CTG CAG GCC CGC TTC ACT TGG CGA GGA GCC CGC CTG Leu Val Leu Tyr Leu Gln Ala Arg Phe Thr Trp Arg Gly Ala Arg Leu 210 215 220 225	968
CTC CGG CCC CTC CTG CAG TTC ACC TTG ATC ATG ATG GCC TTC TAC ACG Leu Arg Pro Leu Leu Gln Phe Thr Leu Ile Met Met Ala Phe Tyr Thr 230 235 240	1016
GGA CTG TCT CGC GTA TCA GAC CAC AAG CAC CAT CCC AGT GAT GTT CTG Gly Leu Ser Arg Val Ser Asp His Lys His His Pro Ser Asp Val Leu 245 250 255	1064
GCA GGA TTT GCT CAA GGA GCC CTG GTG GCC TGC TGC ATA GTT TTC TTC Ala Gly Phe Ala Gln Gly Ala Leu Val Ala Cys Cys Ile Val Phe Phe 260 265 270	1112
GTG TCT GAC CTC TTC AAG ACT AAG ACG ACG CTC TCC CTG CCT GCC CCT Val Ser Asp Leu Phe Lys Thr Lys Thr Thr Leu Ser Leu Pro Ala Pro 275 280 285	1160
GCT ATC CGG AAG GAA ATC CTT TCA CCT GTG GAC ATT ATT GAC AGG AAC Ala Ile Arg Lys Glu Ile Leu Ser Pro Val Asp Ile Ile Asp Arg Asn 290 295 300 305	1208
AAT CAC CAC AAC ATG ATG TAGGTGCCAC CCACCTCCTG AGCTGTTTT Asn His His Asn Met Met 310	1256
GTAAAATGAC TGCTGACAGC AAGTTCTTGC TGCTCTCCAA TCTCATCAGA CAGTAGAATG	1316
TAGGGAAAAA CTTTGCCCCG ACTGATTTTT AAAAAAAA AAAAAA	1362

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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 311 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gln Asn Tyr Lys Tyr Asp Lys Ala Ile Val Pro Glu Ser Lys Asn
1 5 10 15

Gly Gly Ser Pro Ala Leu Asn Asn Asn Pro Arg Arg Ser Gly Ser Lys
20 25 30

Arg Val Leu Leu Ile Cys Leu Asp Leu Phe Cys Leu Phe Met Ala Gly
35 40 45

Leu Pro Phe Leu Ile Ile Glu Thr Ser Thr Ile Lys Pro Tyr His Arg
50 55 60

Gly Phe Tyr Cys Asn Asp Glu Ser Ile Lys Tyr Pro Leu Lys Thr Gly
65 70 75 80

Glu Thr Ile Asn Asp Ala Val Leu Cys Ala Val Gly Ile Val Ile Ala
85 90 95

Ile Leu Ala Ile Ile Thr Gly Glu Phe Tyr Arg Ile Tyr Tyr Leu Lys
100 105 110

Lys Ser Arg Ser Thr Ile Gln Asn Pro Tyr Val Ala Ala Leu Tyr Lys
115 120 125

Gln Val Gly Cys Phe Leu Phe Gly Cys Ala Ile Ser Gln Ser Phe Thr
130 135 140

Asp Ile Ala Lys Val Ser Ile Gly Arg Leu Arg Pro His Phe Leu Ser
145 150 155 160

Val Cys Asn Pro Asp Phe Ser Gln Ile Asn Cys Ser Glu Gly Tyr Ile
165 170 175

Gln Asn Tyr Arg Cys Arg Gly Asp Asp Ser Lys Val Gln Glu Ala Arg
180 185 190

Lys Ser Phe Phe Ser Gly His Ala Ser Phe Ser Met Tyr Thr Met Leu
195 200 205

Tyr Leu Val Leu Tyr Leu Gln Ala Arg Phe Thr Trp Arg Gly Ala Arg
210 215 220

Leu Leu Arg Pro Leu Leu Gln Phe Thr Leu Ile Met Met Ala Phe Tyr
225 230 235 240

Thr Gly Leu Ser Arg Val Ser Asp His Lys His His Pro Ser Asp Val
245 250 255

Leu Ala Gly Phe Ala Gln Gly Ala Leu Val Ala Cys Cys Ile Val Phe
260 265 270

Phe Val Ser Asp Leu Phe Lys Thr Lys Thr Thr Leu Ser Leu Pro Ala
275 280 285

Pro Ala Ile Arg Lys Glu Ile Leu Ser Pro Val Asp Ile Ile Asp Arg
290 295 300

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Asn Asn His His Asn Met Met
305 310

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 4..833

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 4..833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ACC ATG CAG CGG AGG TGG GTC TTC GTG CTG CTC GAC GTG CTG TGC TTA	48
Met Gln Arg Arg Trp Val Phe Val Leu Leu Asp Val Leu Cys Leu	
1 5 10 15	
CTG GTC GCC TCC CTG CCC TTC GCT ATC CTG ACG CTG GTG AAC GCC CCG	96
Leu Val Ala Ser Leu Pro Phe Ala Ile Leu Thr Leu Val Asn Ala Pro	
20 25 30	
TAC AAG CGA GGA TTT TAC TGC GGG GAT GAC TCC ATC CGG TAC CCC TAC	144
Tyr Lys Arg Gly Phe Tyr Cys Gly Asp Asp Ser Ile Arg Tyr Pro Tyr	
35 40 45	
CGT CCA GAT ACC ATC ACC CAC GGG CTC ATG GCT GGG GTC ACC ATC ACG	192
Arg Pro Asp Thr Ile Thr His Gly Leu Met Ala Gly Val Thr Ile Thr	
50 55 60	
GCC ACC GTC ATC CTT GTC TCG GCC GGG GAA GCC TAC CTG GTG TAC ACA	240
Ala Thr Val Ile Leu Val Ser Ala Gly Glu Ala Tyr Leu Val Tyr Thr	
65 70 75	
GAC CGG CTC TAT TCT CGC TCG GAC TTC AAC AAC TAC GTG GCT GCT GTA	288
Asp Arg Leu Tyr Ser Arg Ser Asp Phe Asn Asn Tyr Val Ala Ala Val	
80 85 90 95	
TAC AAG GTG CTG GGG ACC TTC CTG TTT GGG GCT GCC GTG AGC CAG TCT	336
Tyr Lys Val Leu Gly Thr Phe Leu Phe Gly Ala Ala Val Ser Gln Ser	
100 105 110	
CTG ACA GAC CTG GCC AAG TAC ATG ATT GGG CGT CTG AAG CCC AAC TTC	384
Leu Thr Asp Leu Ala Lys Tyr Met Ile Gly Arg Leu Lys Pro Asn Phe	
115 120 125	
CTA GCC GTC TGC GAC CCC GAC TGG AGC CGG GTC AAC TGC TCG GTC TAT	432
Leu Ala Val Cys Asp Pro Asp Trp Ser Arg Val Asn Cys Ser Val Tyr	
130 135 140	
GTG CAG CTG GAG AAG GTG TGC AGG GGA AAC CCT GCT GAT GTC ACC GAG	480
Val Gln Leu Glu Lys Val Cys Arg Gly Asn Pro Ala Asp Val Thr Glu	
145 150 155	
GCC AGG TTG TCT TTC TAC TCG GGA CAC TCT TCC TTT GGG ATG TAC TGC	528
Ala Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Gly Met Tyr Cys	
160 165 170 175	

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-1-

ATG GTG TTC TTG GCG CTG TAT GTG CAG GCA CGA CTC TGT TGG AAG TGG Met Val Phe Leu Ala Leu Tyr Val Gln Ala Arg Leu Cys Trp Lys Trp 180 185 190	576
GCA CGG CTG CTG CGA CCC ACA GTC CAG TTC TTC CTG GTG GCC TTT GCC Ala Arg Leu Leu Arg Pro Thr Val Gln Phe Phe Leu Val Ala Phe Ala 195 200 205	624
CTC TAC GTG GGC TAC ACC CGC GTG TCT GAT TAC AAA CAC CAC TGG AGC Leu Tyr Val Gly Tyr Thr Arg Val Ser Asp Tyr Lys His His Trp Ser 210 215 220	672
GAT GTC CTT GTT GGC CTC CTG CAG GGG GCA CTG GTG GCT GCC CTC ACT Asp Val Leu Val Gly Leu Leu Gln Gly Ala Leu Val Ala Ala Leu Thr 225 230 235	720
GTC TGC TAC ATC TCA GAC TTC TTC AAA GCC CGA CCC CCA CAG CAC TGT Val Cys Tyr Ile Ser Asp Phe Phe Lys Ala Arg Pro Pro Gln His Cys 240 245 250 255	768
CTG AAG GAG GAG GAG CTG GAA CGG AAG CCC AGC CTG TCA CTG ACG TTG Leu Lys Glu Glu Leu Glu Arg Lys Pro Ser Leu Ser Leu Thr Leu 260 265 270	816
ACC CTG GGG CGA GGC TG ACCACAACCA CTTATGGGAT ACCCGCACTC Thr Leu Gly Arg Gly 275	863
TTCTTCCTGA GGCCGGACCC CGCCCAGGCA GGGAGCTGCT GTGAGTCCAG CTGATGCCA CCCAGGTGGT CCCTCCAGCC TGGTTAGGCA CTGAGGGTTC TGGACGGGCT CCAGGAACCC TGGGCTGATG GGAGCAGTGA GCGGTTCCGC TGCCCCCTGC CCTGCACTGG ACCAGGAGTC TGGAGATGCC TGGGTAGCCC TCAGCATTG GAGGGGAACC TGTTCCGTC GGTCCCCAAA TATCCCCTTC TTTTTATGGG GTTAAGGAAG GGACCGAGAG ATCAGATAGT TGCTGTTTG TAAAATGTAA TGTATATGTG GTTTTAGTA AAATAGGGCA CCTGTTTCAC AAAAAAAA AAAAAAA 1232	923 983 1043 1103 1163 1223

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 276 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Gln Arg Arg Trp Val Phe Val Leu Leu Asp Val Leu Cys Leu Leu 1 5 10 15	
Val Ala Ser Leu Pro Phe Ala Ile Leu Thr Leu Val Asn Ala Pro Tyr 20 25 30	
Lys Arg Gly Phe Tyr Cys Gly Asp Asp Ser Ile Arg Tyr Pro Tyr Arg 35 40 45	
Pro Asp Thr Ile Thr His Gly Leu Met Ala Gly Val Thr Ile Thr Ala 50 55 60	

Thr Val Ile Leu Val Ser Ala Gly Glu Ala Tyr Leu Val Tyr Thr Asp
65 70 75 80

Arg Leu Tyr Ser Arg Ser Asp Phe Asn Asn Tyr Val Ala Ala Val Tyr
85 90 95

Lys Val Leu Gly Thr Phe Leu Phe Gly Ala Ala Val Ser Gln Ser Leu
100 105 110

Thr Asp Leu Ala Lys Tyr Met Ile Gly Arg Leu Lys Pro Asn Phe Leu
115 120 125

Ala Val Cys Asp Pro Asp Trp Ser Arg Val Asn Cys Ser Val Tyr Val
130 135 140

Gln Leu Glu Lys Val Cys Arg Gly Asn Pro Ala Asp Val Thr Glu Ala
145 150 155 160

Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Gly Met Tyr Cys Met
165 170 175

Val Phe Leu Ala Leu Tyr Val Gln Ala Arg Leu Cys Trp Lys Trp Ala
180 185 190

Arg Leu Leu Arg Pro Thr Val Gln Phe Phe Leu Val Ala Phe Ala Leu
195 200 205

Tyr Val Gly Tyr Thr Arg Val Ser Asp Tyr Lys His His Trp Ser Asp
210 215 220

Val Leu Val Gly Leu Leu Gln Gly Ala Leu Val Ala Ala Leu Thr Val
225 230 235 240

Cys Tyr Ile Ser Asp Phe Phe Lys Ala Arg Pro Pro Gln His Cys Leu
245 250 255

Lys Glu Glu Glu Leu Glu Arg Lys Pro Ser Leu Ser Leu Thr Leu Thr
260 265 270

Leu Gly Arg Gly
275

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Phe Asp Lys Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Ile Cys
1 5 10 15

Val Leu Leu Ala Gly Leu Pro Phe Ala Ile Leu Thr Ser Arg His Thr
20 25 30

Pro Phe Gln Arg Gly Ile Phe Cys Asn Asp Asp Ser Ile Lys Tyr Pro
35 40 45

Tyr Lys Glu Asp Thr Ile Pro Tyr Ala Leu Leu Gly Gly Ile Val Ile
50 55 60

Pro Phe Cys Ile Ile Val Met Ser Ile Gly Glu Ser Leu Ser Val Tyr
 65 70 75 80
 Phe Asn Val Leu His Ser Asn Ser Phe Val Gly Asn Pro Tyr Ile Ala
 85 90 95
 Thr Ile Tyr Lys Ala Val Gly Ala Phe Leu Phe Gly Val Ser Ala Ser
 100 105 110
 Gln Ser Leu Thr Asp Ile Ala Lys Tyr Thr Ile Gly Ser Leu Arg Pro
 115 120 125
 His Phe Leu Ala Ile Cys Asn Pro Asp Trp Ser Lys Ile Asn Cys Ser
 130 135 140
 Asp Gly Tyr Ile Glu Asp Tyr Ile Cys Gln Gly Asn Glu Glu Lys Val
 145 150 155 160
 Lys Glu Gly Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Ser Met
 165 170 175
 Tyr Cys Met Leu Phe Val Ala Leu Tyr Leu Gln Ala Arg Met Lys Gly
 180 185 190
 Asp Trp Ala Arg Leu Leu Arg Pro Met Leu Gln Phe Gly Leu Ile Ala
 195 200 205
 Phe Ser Ile Tyr Val Gly Leu Ser Arg Val Ser Asp Tyr Lys His His
 210 215 220
 Trp Ser Asp Val Thr Val Gly Leu Ile Gln Gly Ala Ala Met Ala Ile
 225 230 235 240
 Leu Val Ala Leu Tyr Val Ser Asp Phe Phe Lys Asp Thr His Ser Tyr
 245 250 255
 Lys Glu Arg Lys Glu Glu Asp Pro His Thr Thr Leu His Glu Thr Ala
 260 265 270
 Ser Ser Arg Asn Tyr Ser Thr Asn His Glu Pro
 275 280

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Phe Asp Lys Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Leu Cys
 1 5 10 15
 Val Leu Leu Ala Gly Leu Pro Phe Ala Ile Leu Thr Ser Arg His Thr
 20 25 30
 Pro Phe Gln Arg Gly Val Phe Cys Asn Asp Glu Ser Ile Lys Tyr Pro
 35 40 45
 Tyr Lys Glu Asp Thr Ile Pro Tyr Ala Leu Leu Gly Gly Ile Ile Ile
 50 55 60

Pro Phe Ser Ile Ile Val Ile Ile Leu Gly Glu Thr Leu Ser Val Tyr
 65 70 75 80
 Cys Asn Leu Leu His Ser Asn Ser Phe Ile Arg Asn Asn Tyr Ile Ala
 85 90 95
 Thr Ile Tyr Lys Ala Ile Gly Thr Phe Leu Phe Gly Ala Ala Ser
 100 105 110
 Gln Ser Leu Thr Asp Ile Ala Lys Tyr Ser Ile Gly Arg Leu Arg Pro
 115 120 125
 His Phe Leu Asp Val Cys Asp Pro Asp Trp Ser Lys Ile Asn Cys Ser
 130 135 140
 Asp Gly Tyr Ile Glu Tyr Tyr Ile Cys Arg Gly Asn Ala Glu Arg Val
 145 150 155 160
 Lys Glu Gly Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Ser Met
 165 170 175
 Tyr Cys Met Leu Phe Val Ala Leu Tyr Leu Gln Ala Arg Met Lys Gly
 180 185 190
 Asp Trp Ala Arg Leu Leu Arg Pro Thr Leu Gln Phe Gly Leu Val Ala
 195 200 205
 Val Ser Ile Tyr Val Gly Leu Ser Arg Val Ser Asp Tyr Lys His His
 210 215 220
 Trp Ser Asp Val Leu Thr Gly Leu Ile Gln Gly Ala Leu Val Ala Ile
 225 230 235 240
 Leu Val Ala Val Tyr Val Ser Asp Phe Phe Lys Glu Arg Thr Ser Phe
 245 250 255
 Lys Glu Arg Lys Glu Glu Asp Ser His Thr Thr Leu His Glu Thr Pro
 260 265 270
 Thr Thr Gly Asn His Tyr Pro Ser Asn His Gln Pro
 275 280

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Phe Asp Lys Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Leu Cys
 1 5 10 15
 Val Leu Leu Ala Ser Met Pro Met Ala Val Leu Lys Leu Gly Gln Ile
 20 25 30
 Tyr Pro Phe Gln Arg Gly Phe Phe Cys Lys Asp Asn Ser Ile Asn Tyr
 35 40 45
 Pro Tyr His Asp Ser Thr Ala Ala Ser Thr Val Leu Ile Leu Val Gly
 50 55 60

Val Gly Leu Pro Val Ser Ser Ile Ile Leu Gly Glu Thr Leu Ser Val
 65 70 75 80
 Tyr Cys Asn Leu Leu His Ser Asn Ser Phe Ile Arg Asn Asn Tyr Ile
 85 90 95
 Ala Thr Ile Tyr Lys Ala Ile Gly Thr Phe Leu Phe Gly Ala Ala Ala
 100 105 110
 Ser Gln Ser Leu Thr Asp Ile Ala Lys Tyr Ser Ile Gly Arg Leu Arg
 115 120 125
 Pro His Phe Leu Asp Val Cys Asp Pro Asp Trp Ser Lys Ile Asn Cys
 130 135 140
 Ser Asp Gly Tyr Ile Glu Tyr Tyr Ile Cys Arg Gly Asn Ala Glu Arg
 145 150 155 160
 Val Lys Glu Gly Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Ser
 165 170 175
 Met Tyr Cys Met Leu Phe Val Ala Leu Tyr Leu Gln Ala Arg Met Lys
 180 185 190
 Gly Asp Trp Ala Arg Leu Leu Arg Pro Thr Leu Gln Phe Gly Leu Val
 195 200 205
 Ala Val Ser Ile Tyr Val Gly Leu Ser Arg Val Ser Asp Tyr Lys His
 210 215 220
 His Trp Ser Asp Val Leu Thr Gly Leu Ile Gln Gly Ala Leu Val Ala
 225 230 235 240
 Ile Leu Val Ala Val Tyr Val Ser Asp Phe Phe Lys Glu Arg Thr Ser
 245 250 255
 Phe Lys Glu Arg Lys Glu Glu Asp Ser His Thr Thr Leu His Glu Thr
 260 265 270
 Pro Thr Thr Gly Asn His Tyr Pro Ser Asn His Gln Pro
 275 280 285

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Gln Asn Tyr Lys Tyr Asp Lys Ala Ile Val Pro Glu Ser Lys Asn
 1 5 10 15
 Gly Gly Ser Pro Ala Leu Asn Asn Asn Pro Arg Arg Ser Gly Ser Lys
 20 25 30
 Arg Val Leu Leu Ile Cys Leu Asp Leu Phe Cys Leu Phe Met Ala Gly
 35 40 45
 Leu Pro Phe Leu Ile Ile Glu Thr Ser Thr Ile Lys Pro Tyr His Arg
 50 55 60

Gly Phe Tyr Cys Asn Asp Glu Ser Ile Lys Tyr Pro Leu Lys Thr Gly
65 70 75 80

Glu Thr Ile Asn Asp Ala Val Leu Cys Ala Val Gly Ile Val Ile Ala
85 90 95

Ile Leu Ala Ile Ile Thr Gly Glu Phe Tyr Arg Ile Tyr Tyr Leu Lys
100 105 110

Lys Ser Arg Ser Thr Ile Gln Asn Pro Tyr Val Ala Ala Leu Tyr Lys
115 120 125

Gln Val Gly Cys Phe Leu Phe Gly Cys Ala Ile Ser Gln Ser Phe Thr
130 135 140

Asp Ile Ala Lys Val Ser Ile Gly Arg Leu Arg Pro His Phe Leu Ser
145 150 155 160

Val Cys Asn Pro Asp Phe Ser Gln Ile Asn Cys Ser Glu Gly Tyr Ile
165 170 175

Gln Asn Tyr Arg Cys Arg Gly Asp Asp Ser Lys Val Gln Glu Ala Arg
180 185 190

Lys Ser Phe Phe Ser Gly His Ala Ser Phe Ser Met Tyr Thr Met Leu
195 200 205

Tyr Leu Val Leu Tyr Leu Gln Ala Arg Phe Thr Trp Arg Gly Ala Arg
210 215 220

Leu Leu Arg Pro Leu Leu Gln Phe Thr Leu Ile Met Met Ala Phe Tyr
225 230 235 240

Thr Gly Leu Ser Arg Val Ser Asp His Lys His His Pro Ser Asp Val
245 250 255

Leu Ala Gly Phe Ala Gln Gly Ala Leu Val Ala Cys Cys Ile Val Phe
260 265 270

Phe Val Ser Asp Leu Phe Lys Thr Lys Thr Thr Leu Ser Leu Pro Ala
275 280 285

Pro Ala Ile Arg Lys Glu Ile Leu Ser Pro Val Asp Ile Ile Asp Arg
290 295 300

Asn Asn His His Asn Met Met
305 310

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Gln Arg Arg Trp Val Phe Val Leu Leu Asp Val Leu Cys Leu Leu
1 5 10 15

Val Ala Ser Leu Pro Phe Ala Ile Leu Thr Leu Val Asn Ala Pro Tyr
20 25 30

Lys Arg Gly Phe Tyr Cys Gly Asp Asp Ser Ile Arg Tyr Pro Tyr Arg
 35 40 45

Pro Asp Thr Ile Thr His Gly Leu Met Ala Gly Val Thr Ile Thr Ala
 50 55 60

Thr Val Ile Leu Val Ser Ala Gly Glu Ala Tyr Leu Val Tyr Thr Asp
 65 70 75 80

Arg Leu Tyr Ser Arg Ser Asp Phe Asn Asn Tyr Val Ala Ala Val Tyr
 85 90 95

Lys Val Leu Gly Thr Phe Leu Phe Gly Ala Ala Val Ser Gln Ser Leu
 100 105 110

Thr Asp Leu Ala Lys Tyr Met Ile Gly Arg Leu Lys Pro Asn Phe Leu
 115 120 125

Ala Val Cys Asp Pro Asp Trp Ser Arg Val Asn Cys Ser Val Tyr Val
 130 135 140

Gln Leu Glu Lys Val Cys Arg Gly Asn Pro Ala Asp Val Thr Glu Ala
 145 150 155 160

Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Gly Met Tyr Cys Met
 165 170 175

Val Phe Leu Ala Leu Tyr Val Gln Ala Arg Leu Cys Trp Lys Trp Ala
 180 185 190

Arg Leu Leu Arg Pro Thr Val Gln Phe Phe Leu Val Ala Phe Ala Leu
 195 200 205

Tyr Val Gly Tyr Thr Arg Val Ser Asp Tyr Lys His His Trp Ser Asp
 210 215 220

Val Leu Val Gly Leu Leu Gln Gly Ala Leu Val Ala Ala Leu Thr Val
 225 230 235 240

Cys Tyr Ile Ser Asp Phe Phe Lys Ala Arg Pro Pro Gln His Cys Leu
 245 250 255

Lys Glu Glu Glu Leu Glu Arg Lys Pro Ser Leu Ser Leu Thr Leu Thr
 260 265 270

Leu Gly Arg Gly
 275

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGCTCTAGAT ATTAATAGTA ATCAATTAC

29

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCTCACGCAT GCACCATGGT AATAGC

26

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGTGCATGCG TGAGGGCTCCG GTGC

24

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTAGTTTCA CGGTACCTGA AATGGAAG

28

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGCATGGTAC CATGTTGAC AAGACGCGC

30

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

9

41
-19-

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CATATGTAGT ATTCAATGTA ACC

23

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGATGGCTAG CATGCAGAGA AGATGGGTCT TCGTGCTGCT CGACGTG

47

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AGTGCAGGAT CCCATAAGTG GTTG

24